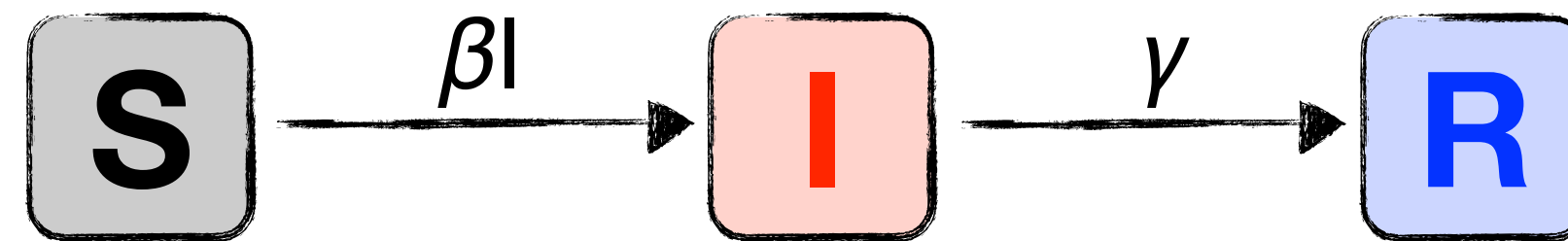


The fundamental model of disease transmission: the SIR model

If we describe how an **individual** progresses through disease...



The **S** → **I** transition depends on **infectiousness** (β) and the **number of infectious people** (**I**)

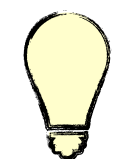
The **I** → **R** transition depends on the **recovery rate** (γ)

To translate this diagram into equations,
multiply the **rates** over the arrows by the **states** at the arrow's tail:

$$\frac{dS}{dt} = -\beta IS$$

$$\frac{dI}{dt} = \beta IS - \gamma I$$

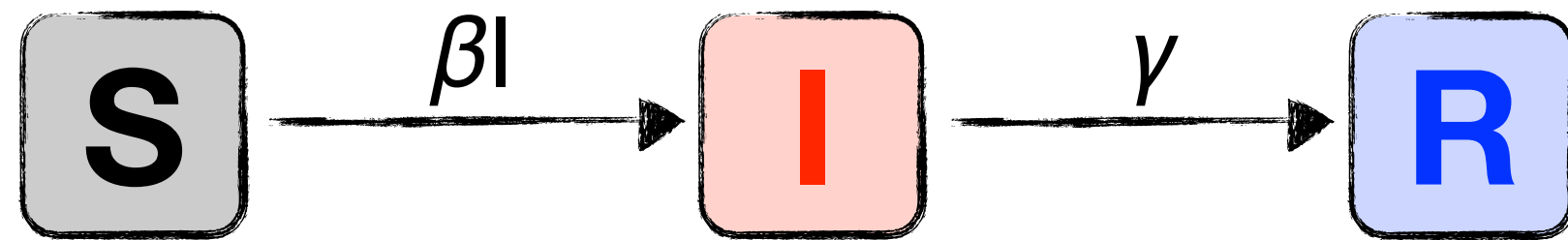
$$\frac{dR}{dt} = \gamma I$$



Solving these equations means asking: how do the number of people in S, I, and R vary over time, given the individual-level values we've put into the model?

The fundamental model of disease transmission: the SIR model

We can't solve these equations by hand, so we use computer simulations:



How many people do we expect an **infectious** person to infect?

They'll infect β people per unit of time, until they recover – which happens at rate γ .

So, over the entire course of their infection, we expect them to infect β/γ people.

This is the **basic reproduction number (R_0)**: the expected number of people that an infectious person will infect in a totally susceptible population.

Let's imagine a disease where a person infects one person per week ($\beta = 1$) and it takes two weeks to recover ($\gamma = 1/2$).

The reproduction number is then

$$R_0 = \beta/\gamma = 1/(1/2) = 2$$

